

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: Regents of the University of Minnesota
- (B) STREET: Morrill Hall, 100 Church Street, S.E.
- (C) CITY: Minneapolis
- (D) STATE: Minnesota
- (E) COUNTRY: United States of America
- (F) POSTAL CODE (ZIP): 55415-1226

## (ii) TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE

## (iii) NUMBER OF SEQUENCES: 13

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 07-JUN-1996
- (C) CLASSIFICATION:

## (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/480,261
- (B) FILING DATE: 07-JUN-1995
- (C) CLASSIFICATION:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCATCACGGG TGGATTCTTG AAACAGGTG  
29

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATCACGCC CCCCGTCGAC GATAAAATAG TTGCTAAGCT ACAAGCT  
47

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA  
60

TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA  
120

ATTTCATAA ATATTAAATA ATAATTAAAA ATAAATAAT AAATAATTAA TC  
172

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA  
60

TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA  
120

ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC  
172

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA  
60

TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA  
120

ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC  
172

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA  
60

TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA  
120

ATTTCCTATA ATATTAAATA ATAATTAAAA ATAAAATAAT AAATAATTAA TC  
172

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA  
60

TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA  
120

ATTTCCTATA ATATTAAATA ATAATTAAAA ATAAAATAAT AAATAATTAA TC  
172

75

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA  
60

TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA  
120

ATTTCATATA ATATTAAATA ATAATTAAAA ATAAATAAT AAATAATTAA TC  
172

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA  
60

TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA  
120

ATTTCATATA ATATTAAATA ATAATTAAAA ATAAATAAT AAATAATTAA TC  
172

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA  
60

TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA  
120

ATTTCATATA ATATTAAATA ATAATTAAAA ATAAATAAT AAATAATTAA TC  
172

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCATCACGGG TGGATCCTTG AAACAGGTGC A  
31

77

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 828..1583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATCACGCA TCACTCATGT TTGACAGCTT ATCATCGATA AGCTTACTTT TCGAATCAGG  
60

TCTATCCTTG AAACAGGTGC AACATAGATT AGGGCATGGA GATTTACCAG ACAACTATGA  
120

ACGTATATAC TCACATCACG CAATCGGCAA TTGATGACAT TGGAAGTAAA TTCAATCAAT  
180

TTGTTACTAA CAAGCAACTA GATTGACAAC TAATTCTCAA CAAACGTTAA TTTAACAACA  
240

TTCAAGTAAC TCCCACCAGC TCCATCAATG CTTACCGTAA GTAATCATAA CTTACTAAAA  
300

CCTTGTTACA TCAAGGTTTT TTCTTTTGT CTTGTTTCATG AGTTACCATA ACTTTCTATA  
360

TTATTGACAA CTAAATTGAC AACTCTTCAA TTATTTTCT GTCTACTCAA AGTTTTCTTC  
420

ATTTGATATA GTCTAATTCC ACCATCACTT CTTCCACTCT CTCTACCGTC ACAACTTCAT  
480

CATCTCTCAC TTTTTCGTGT GGTAACACAT AATCAAATAT CTTCCGTTT TTACGCACTA  
540

TCGCTACTGT GTCACCTAAA ATATACCCCT TATCAATCGC TTCTTTAAAC TCATCTATAT  
600

ATAACATATT TCATCCTCCT ACCTATCTAT TCGTAAAAAG ATAAAAATAA CTATTGTTTT  
660

TTTTGTTATT TTATAATAAA ATTATTAATA TAAGTTAATG TTTTTTAAAA ATATACAATT  
720

TTATTCTATT TATAGTTAGC TATTTTTTCA TTGTTAGTAA TATTGGTGAA TTGTAATAAC  
780

CTTTTTTAAAT CTAGAGGAGA ACCCAGATAT AAAATGGAGG AATATTA ATG GAA AAC  
836

Met Glu Asn  
1

AAT AAA AAA GTA TTG AAG AAA ATG GTA TTT TTT GTT TTA GTG ACA TTT  
884

Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu Val Thr Phe  
5 10 15

CTT GGA CTA ACA ATC TCG CAA GAG GTA TTT GCT CAA CAA GAC CCC GAT  
 932  
 Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln Asp Pro Asp  
 20 25 30 35

CCA AGC CAA CTT CAC AGA TCT AGT TTA GTT AAA AAC CTT CAA AAT ATA  
 980  
 Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile  
 40 45 50

TAT TTT CTT TAT GAG GGT GAC CCT GTT ACT CAC GAG AAT GTG AAA TCT  
 1028  
 Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser  
 55 60 65

GTT GAT CAA CTT TTA TCT CAC CAT TTA ATA TAT AAT GTT TCA GGG CCA  
 1076  
 Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro  
 70 75 80

AAT TAT GAT AAA TTA AAA ACT GAA CTT AAG AAC CAA GAG ATG GCA ACT  
 1124  
 Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr  
 85 90 95

TTA TTT AAG GAT AAA AAC GTT GAT ATT TAT GGT GTA GAA TAT TAC CAT  
 1172  
 Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His  
 100 105 110 115

CTC TGT TAT TTA TGT GAA AAT GCA GAA AGG AGT GCA TGT ATC TAC GGA  
 1220  
 Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly  
 120 125 130

GGG GTA ACA AAT CAT GAA GGG AAT CAT TTA GAA ATT CCT AAA AAG ATA  
 1268  
 Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile  
 135 140 145

GTC GTT AAA GTA TCA ATC GAT GGT ATC CAA AGC CTA TCA TTT GAT ATT  
 1316  
 Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile  
 150 155 160

GAA ACA AAT AAA AAA ATG GTA ACT GCT CAA GAA TTA GAC TAT AAA GTT  
 1364  
 Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val  
 165 170 175

AGA AAA TAT CTT ACA GAT AAT AAG CAA CTA TAT ACT AAT GGA CCT TCT  
 1412  
 Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser  
 180 185 190 195

AAA TAT GAA ACT GGA TAT ATA AAG TTC ATA CCT AAG AAT AAA GAA AGT  
 1460  
 Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu Ser  
 200 205 210

TTT TGG TTT GAT TTT TTC CCT GAA CCA GAA TTT ACT CAA TCT AAA TAT  
 1508  
 Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr  
 215 220 225



CTT ATG ATA TAT AAA GAT AAT GAA ACG CTT GAC TCA AAC ACA AGC CAA

1556

Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln

230

235

240

ATT GAA GTC TAC CTA ACA ACC AAG TAA CTTTTTGCTT TTGGCAACCT

1603

Ile Glu Val Tyr Leu Thr Thr Lys \*

245

250

TACCTACTGC TGGATTAGA AATTTTATTG CAATTCTTTT ATTAATGTAA AAACCGCTCA

1663

TTTGATGAGC GGTTTTGTCT TATCTAAAGG AGCTTTACCT CCTAATGCTG CAAAATTTTA

1723

AATGTTGGAT TTTTGTATTT GTCTATTGTA TTTGATGGGT AATCCCATTT TTCGACAGAC

1783

ATCGTCGTGC CACCTCTAAC ACCAAAATCA TAGACAGGAG CTTGTAGCTT AGCAACTATT

1843

TTATCGTC

1851

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Met Glu Asn Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu
 1           5           10           15
Val Thr Phe Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln
          20           25           30
Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu
          35           40           45
Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn
          50           55           60
Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val
          65           70           75           80
Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu
          85           90           95
Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu
          100          105          110
Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys
          115          120          125
Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro
          130          135          140
Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser
          145          150          155          160
Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp
          165          170          175
Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn
          180          185          190
Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn
          195          200          205
Lys Glu Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln
          210          215          220
Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn
          225          230          235          240
Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys *
          245          250

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